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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=1; day=20; hr=11; min=41; sec=50; ms=556;]

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Application No: 10580635 Version No: 2.0

Input Set:**Output Set:**

Started: 2010-01-04 17:43:00.033
Finished: 2010-01-04 17:43:03.054
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 21 ms
Total Warnings: 30
Total Errors: 0
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

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Output Set:

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Total Warnings: 30
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
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W 213	Artificial or Unknown found in <213> in SEQ ID (25) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Pastan, Ira H.
Ho, Mitchell
Bang, Sook-Hee
The Government of the United States
as represented by The Secretary of the
Department of Health and Human Services

<120> Mutated Anti-CD22 Antibodies and Immunoconjugates

<130> 015280-500100US

<140> 10580635
<141> 2010-01-04

<150> US 60/525,371
<151> 2003-11-25

<150> WO PCT/US04/39617
<151> 2004-11-24

<160> 30

<170> PatentIn Ver. 2.1

<210> 1
<211> 321
<212> DNA
<213> Mus sp.

<220>
<223> RFB4 mouse IgG1 anti-human CD22 monoclonal
antibody light chain variable region (VL)

<220>
<221> CDS
<222> (1)..(321)
<223> RFB4 mouse IgG1 anti-human CD22 monoclonal
antibody light chain variable region (VL)

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Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
gac aga gtc acc att agt tgc agg gca agt cag gac att agc aat tat 96
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30
tta aac tgg tat cag cag aaa cca gat gga act gtt aaa ctc ctg atc 144
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45
tac tac aca tca ata tta cac tca gga gtc cca tca agg ttc agt ggc 192
Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly

50	55	60	
agt ggg tct gga aca gat tat tct ctc acc att agc aac ctg gag caa			240
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln			
65	70	75	80
gaa gat ttt gcc act tac ttt tgc caa cag ggt aat acg ctt ccg tgg			288
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp			
	85	90	95
acg ttc ggt gga ggc acc aag ctg gaa atc aaa			321
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys			
	100	105	

<210> 2

<211> 107

<212> PRT

<213> Mus sp.

<220>

<223> RFB4 mouse IgG1 anti-human CD22 monoclonal
antibody light chain variable region (VL)

<400> 2

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly			
1	5	10	15
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr			
	20	25	30
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile			
	35	40	45
Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly			
	50	55	60
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln			
65	70	75	80
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp			
	85	90	95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys			
	100	105	

<210> 3

<211> 369

<212> DNA

<213> Mus sp.

<220>

<223> RFB4 mouse IgG1 anti-human CD22 monoclonal
antibody heavy chain variable region (VH)

<220>

<221> CDS

<222> (1)..(369)

<223> RFB4 mouse IgG1 anti-human CD22 monoclonal
antibody heavy chain variable region (VH)

<400> 3

gaa gtg cag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc gct ttc agt atc tat 96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
20 25 30

gac atg tct tgg gtt cgc cag act ccg gag aag agg ctg gag tgg gtc 144
Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

gca tac att agt agt ggt ggt ggt acc acc tac tat cca gac act gtg 192
Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60

aag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc ctg tac 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg agc agt ctg aag tct gag gac aca gcc atg tat tac tgt 288
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

gca aga cat agt ggc tac ggt agt agc tac ggg gtt ttg ttt gct tac 336
Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

tgg ggc caa ggg act ctg gtc act gtc tct gca 369
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 4

<211> 123

<212> PRT

<213> Mus sp.

<220>

<223> RFB4 mouse IgG1 anti-human CD22 monoclonal
antibody heavy chain variable region (VH)

<400> 4

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 5

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:carboxyl
terminal fragment binding KDEL recycling receptor
for transport of construct into cytosol from
endoplasmic reticulum

<400> 5

Lys Asp Glu Leu

1

<210> 6

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:carboxyl
terminal fragment binding KDEL recycling receptor
for transport of construct into cytosol from
endoplasmic reticulum

<400> 6

Arg Glu Asp Leu

1

<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:RFB4 variable
light chain (VL) complementarity determining

region 1 (CDR1)

<400> 7

Gln Asp Ile His Gly Tyr
1 5

<210> 8

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:RFB4 variable
light chain (VL) complementarity determining
region 1 (CDR1)

<400> 8

Gln Asp Ile Gly Arg Tyr
1 5

<210> 9

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:RFB4 variable
light chain (VL) complementarity determining
region 1 (CDR1)

<400> 9

Gln Asp Ile Arg Gly Tyr
1 5

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:RFB4 variable
light chain (VL) complementarity determining
region 1 (CDR1)

<400> 10

Gln Asp Ile Ala Arg Tyr
1 5

<210> 11

<211> 3

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:RFB4 variable
light chain (VL) complementarity determining
region 2 (CDR2)

<400> 11
Tyr Thr Ser
1

<210> 12
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:RFB4 variable
light chain (VL) complementarity determining
region 3 (CDR3)

<400> 12
Gln Gln Gly Asn Thr Leu Pro Trp Thr
1 5

<210> 13
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:RFB4 variable
heavy chain (VH) complementarity determining
region 1 (CDR1)

<400> 13
Gly Phe Ala Phe Ser Ile Tyr Asp
1 5

<210> 14
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:RFB4 variable
heavy chain (VH) complementarity determining
region 2 (CDR2)

<400> 14
Ile Ser Ser Gly Gly Gly Thr Thr
1 5

<210> 15
<211> 16

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RFB4 variable
 heavy chain (VH) complementarity determining
 region 3 (CDR3)

 <400> 15
 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
 1 5 10 15

 <210> 16
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RFB4 variable
 heavy chain (VH) complementarity determining
 region 3 (CDR3)

 <400> 16
 Ala Arg His Ser Gly Tyr Gly Thr His Trp Gly Val Leu Phe Ala Tyr
 1 5 10 15

 <210> 17
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RFB4 variable
 heavy chain (VH) complementarity determining
 region 3 (CDR3)

 <400> 17
 Ala Arg His Ser Gly Tyr Gly Tyr Asn Trp Gly Val Leu Phe Ala Tyr
 1 5 10 15

 <210> 18
 <211> 16
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:RFB4 variable
 heavy chain (VH) complementarity determining
 region 3 (CDR3)

 <400> 18
 Ala Arg His Ser Gly Tyr Gly Thr Thr Trp Gly Val Leu Phe Ala Tyr
 1 5 10 15

<210> 19
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:RFB4 variable
heavy chain (VH) complementarity determining
region 3 (CDR3)

<400> 19
Ala Arg His Ser Gly Tyr Gly Ser Thr Tyr Gly Val Leu Phe Ala Tyr
1 5 10 15

<210> 20
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutated RFB4 VL
chain

<400> 20
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile His Gly Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 21
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutated RFB4 VH
chain

<400> 21

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
20 25 30
Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Arg His Ser Gly Tyr Gly Thr His Trp Gly Val Leu Phe Ala Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 22

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Pseudomonas
exotoxin A cytotoxic fragment PE38 translocating
and ADP ribosylating domains

<400> 22

Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro
1 5 10 15
Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu
20 25 30
Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala
35 40 45
Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
50 55 60
Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
65 70 75 80
Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
85 90 95
Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn
100 105 110

Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr
 115 120 125
 Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg
 130 135 140
 Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln
 145 150 155 160
 Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu
 165 170 175
 Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln
 180 185 190
 Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala
 195 200 205
 Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg
 210 215 220
 Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu
 225 230 235 240
 Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala
 245 250 255
 Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp
 260 265 270
 Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu
 275 280 285
 Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro
 290 295 300
 Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro
 305 310 315 320
 Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro
 325 330 335
 Gly Lys Pro Pro Arg Glu Asp Leu Lys
 340 345

<210> 23

<211> 345

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Pseudomonas exotoxin A
 cytotoxic fragment PE38 translocating and ADP ribosylating
 domains with Arg at position 222 of PE38 (position 490 of
 Pseudomonas exotoxin A) mutated to Ala

<400> 23

Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro
1 5 10 15

Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu
20 25 30

Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala
35 40 45

Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu
50 55 60

Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln
65 70 75 80

Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu
85